CLAIM AMENDMENTS

1. *(Currently Amended)* A method of identifying a nucleic acid in a sample, comprising:

a) combining the sample with a polynucleotide probe ~~comprising a sequence identical or complementary to at least 10 consecutive nucleotides contained in SEQ ID NO:224,~~ such that the probe hybridizes specifically to the nucleic acid if the nucleic acid encodes human telomerase reverse transcriptase (hTRT) or fragment thereof;

b) detecting any hybrid formed as a result of a); and

c) identifying the nucleic acid as encoding ~~at least a portion of human telomerase reverse transcriptase (hTRT)~~ hTRT or fragment thereof if the hybrid is detected;

wherein the probe hybridizes specifically to a DNA having the sequence of the hTRT encoding region of SEQ. ID NO:224 at 5°C to 25°C below T_m in aqueous solution at 1 M NaCl;

wherein T_m is the melting temperature of double-stranded DNA having the sequence of said encoding region under the same reaction conditions.

2. *(Currently Amended)* A method of detecting a nucleic acid that encodes hTRT or fragment thereof in a sample, comprising:

a) combining the sample with a polynucleotide probe such that the probe hybridizes specifically to a nucleic acid comprising at least 100 consecutive nucleotides contained in SEQ ID NO:224 if present in the sample; and

b) detecting any hybrid formed as a result of a);

wherein the polynucleotide probe ~~comprises~~ consists essentially of a sequence identical or complementary to ~~at least~~ 25 or more consecutive nucleotides ~~contained in~~ from the hTRT encoding region of SEQ ID NO:224.

3. *(Original)* The method of claim 2, wherein the hTRT nucleic acid is human genomic DNA.

4. *(Currently Amended)* The method of claim 2, wherein the hTRT nucleic acid is ~~human mRNA~~ mRNA or cDNA.

5. *(Currently Amended)* The method of claim 2, wherein the hTRT nucleic acid comprises ~~at least~~ 250 or more nucleotides of SEQ ID NO:224.

6. *(Currently Amended)* The method of claim 2, wherein the hTRT nucleic acid comprises ~~at least~~ 500 or more nucleotides of SEQ ID NO:224.

7. *(Currently Amended)* The method of claim 2, wherein the probe comprises a sequence identical or complementary to ~~at least~~ 30 or more consecutive nucleotides ~~contained in~~ from the hTRT encoding region of SEQ ID NO:224.

8. *(Currently Amended)* The method of claim 2, wherein the probe comprises a sequence identical or complementary to ~~at least~~ 50 or more consecutive nucleotides ~~contained in~~ from the hTRT encoding region of SEQ ID NO:224.

9. *(Currently Amended)* The method of claim 2, wherein the probe comprises a sequence identical or complementary to ~~at least~~ 100 or more consecutive nucleotides ~~contained in~~ from the hTRT encoding region of SEQ ID NO:224.

10. *(Original)* The method of claim 2, wherein the probe comprises a sequence not contained in SEQ. ID NO:62.

11. *(Original)* The method of claim 9, wherein the probe comprises a sequence not contained in SEQ. ID NO:62.

12. *(Original)* The method of claim 2, wherein the sample is a human biological sample.

13. *(Currently Amended)* A method of identifying a nucleic acid in a sample, comprising:

a) combining the sample with a polynucleotide primer ~~containing a sequence identical or complementary to at least 10 consecutive nucleotides contained in SEQ ID NO:224,~~ under conditions that the primer ~~amplifies~~ specifically primes amplification of the nucleic acid if the nucleic acid encodes human telomerase reverse transcriptase (hTRT) or fragment thereof;

b) detecting any amplification product formed as a result of a); and

c) identifying the nucleic acid as encoding ~~at least a portion of~~ hTRT or fragment thereof if the amplification product is detected ;

wherein the primer hybridizes specifically to a DNA having the sequence of the hTRT encoding region of SEQ. ID NO:224 at 5°C to 25°C below T_m in aqueous solution at 1 M NaCl;

wherein T_m is the melting temperature of double-stranded DNA having the sequence of said encoding region under the same reaction conditions.

14. *(Currently Amended)* A method of detecting a nucleic acid encoding ~~at least a portion of~~ hTRT or fragment thereof in a sample, comprising:

a) combining the sample with ~~a polynucleotide primer such that the primer amplifies~~ polynucleotide primers so as to prime amplification of nucleic acid encoding ~~at least a portion of~~ hTRT or fragment thereof if present in the sample; and

b) detecting any amplified product formed as a result of a);

wherein the ~~polynucleotide primer comprises~~ each of said primers consists essentially of a sequence identical or complementary to ~~at least~~ 15 or more consecutive nucleotides ~~contained in~~ from the hTRT encoding region of SEQ ID NO:224.

15. *(Currently Amended)* The method of claim 14, wherein ~~the polynucleotide primer comprises~~ each of said primers consists essentially of a sequence identical or complementary to ~~at least~~ 30 or more consecutive nucleotides ~~contained in~~ from the hTRT encoding region of SEQ ID NO:224.

16. *(Currently Amended)* The method of claim 14, wherein ~~the polynucleotide primer comprises~~ each of said primers consists essentially of a sequence identical or complementary to ~~at least~~ 50 or more consecutive nucleotides ~~contained in~~ from the hTRT encoding region of SEQ ID NO:224.

17. *(Original)* The method of claim 14, wherein the sample is a human biological sample.

18. *(Original)* The method of claim 14, wherein the sample comprises human genomic DNA.

19. *(Currently Amended)* The method of claim 14, wherein the sample comprises ~~human mRNA~~ hTRT mRNA or cDNA.

20. *CANCELLED.*

21. *(Original)* The method of claim 14, wherein the ~~primer comprises~~ primers comprise a sequence not contained in SEQ. ID NO:62.

22. *CANCELLED*

23. *(Withdrawn) (Currently Amended)* A combination of oligonucleotide primers for PCR amplification for use in detecting an hTRT nucleic acid according to claim 14, ~~comprising a first primer that hybridizes to a polynucleotide consisting of SEQ ID NO:224 under stringent amplification conditions, and a second primer that hybridizes to the complement of said nucleic acid under stringent amplification conditions~~ wherein each primer consists essentially of a sequence identical or complementary to 15 or more consecutive nucleotides from the hTRT encoding region of SEQ ID NO:224.

24. *(Withdrawn)* The combination of primers of claim 23, wherein ~~either~~ each primer ~~comprises between~~ consists of 15-30 nucleotides.

25. *(Withdrawn)* The combination of primers of claim 23, wherein ~~either~~ each primer ~~comprises between~~ consists of 20-25 nucleotides.

26. *(Withdrawn)* The combination of primers of claim 23, wherein 50% or more of the nucleotides of ~~either~~ each primer are guanine and/or cytosine.

27. *(Withdrawn) (Currently Amended)* A PCR product ~~that hybridizes under stringent conditions to a polynucleotide having a sequence consisting of~~ formed while undertaking the detection method of claim 14, comprising 15 or more contiguous nucleotides of the hTRT encoding region of SEQ ID NO:224 or its complement.

28. *(Withdrawn) (Currently Amended)* A hybridization complex formed while undertaking the detection method of claim 2, comprising:

a) one strand of a cellular hTRT nucleic acid; and

b) one strand of a nucleic acid ~~comprising a recombinant or synthetic fragment of hTERT, wherein said fragment of hTRT comprises at least 10 contiguous nucleotides of~~ consisting essentially of 25 or more consecutive nucleotides of the hTRT encoding region of SEQ ID NO:224 or its complement.

29. *(Withdrawn)* The hybridization complex of claim 28, wherein the hTRT nucleic acid is an hTRT mRNA.

30. *(Withdrawn)* The hybridization complex of claim 28, wherein the hTRT nucleic acid is an hTRT cDNA.

31. *(Withdrawn)* The hybridization complex of claim 28, wherein the fragment comprises ~~at least~~ 20 ~~contiguous~~ or more consecutive nucleotides of SEQ ID NO:224 or its complement.

32. *(Withdrawn) (Currently Amended)* The hybridization complex of claim 28, wherein the fragment ~~comprises 10-100 contiguous~~ 100 or more consecutive nucleotides of SEQ ID NO:224 or its complement.

33. *(Withdrawn)* The hybridization complex of claim 28, wherein said hybridization complex is a DNA:DNA complex.

34. *(Withdrawn)* The hybridization complex of claim 28, wherein said hybridization complex is a DNA:RNA complex.

35. *(New)* The method of claim 1, wherein a) comprises combining the sample with the probe at 5°C to 25°C below T_m in aqueous solution at 1 M NaCl.

36. *(New)* The method of claim 1, wherein the hTRT nucleic acid is hTRT mRNA or cDNA.

37. *(New)* The method of claim 1, wherein the probe comprises a sequence identical or complementary to 100 or more consecutive nucleotides from the hTRT encoding region of SEQ ID NO:224.

38. *(New)* The method of claim 1, wherein the probe comprises a sequence not contained in SEQ. ID NO:62.

39. *(New)* The method of claim 1, wherein the sample has been taken from a patient, and the method further comprises determining or assessing a tumor in the patient according to whether a nucleic acid encoding hTRT or an hTRT fragment is detected.

40. *(New)* The method of claim 2, wherein the sample has been taken from a patient, and the method further comprises determining or assessing a tumor in the patient according to whether said nucleic acid hybrid is detected.

41. *(New)* The method of claim 13, wherein a) comprises combining the sample with the primer at 5°C to 25°C below T_m in aqueous solution at 1 M NaCl.

42. *(New)* The method of claim 13, wherein the hTRT nucleic acid is mRNA or cDNA.

43. *(New)* The method of claim 13, wherein the primer comprises a sequence identical or complementary to 30 or more consecutive nucleotides from the hTRT encoding region of SEQ ID NO:224.

44. *(New)* The method of claim 13, wherein the primer comprises a sequence not contained in SEQ. ID NO:62.

45. *(New)* The method of claim 13, wherein the sample has been taken from a patient, and the method comprises determining or assessing a tumor in the patient according to whether a nucleic acid encoding hTRT or an hTRT fragment is detected.

46. *(New)* The method of claim 14, wherein the sample has been taken from a patient, and the method comprises determining or assessing a tumor in the patient according to whether said amplification product is formed.